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# 2

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,775

DATE: 12/12/2001

TIME: 14:16:48

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112001\I002775.raw

ENTERED

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3 <110> APPLICANT: Gordon Freeman
4      Vassiliki Boussiotis
5      Tatyana Chernova
6      Nelly Malenkovich
8 <120> TITLE OF INVENTION: NOVEL B7-4 MOLECULES AND USES THEREFOR
10 <130> FILE REFERENCE: GNN-004ADV
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/002,775
C--> 13 <141> CURRENT FILING DATE: 2001-11-02
15 <150> PRIOR APPLICATION NUMBER: US 09/644,934
16 <151> PRIOR FILING DATE: 2000-08-23
18 <150> PRIOR APPLICATION NUMBER: 60/150,390
19 <151> PRIOR FILING DATE: 1999-08-23
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: PatentIn Ver. 2.0
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26 <211> LENGTH: 968
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
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32 <222> LOCATION: (59)..(793)
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37 atg agg ata ttt gct gtc ttt ata ttc atg acc tac tgg cat ttg ctg      106
38 Met Arg Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu
39 1 5 10 15
41 aac gca ttt act gtc acg gtt ccc aag gac cta tat gtg gta gag tat      154
42 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
43 20 25 30
45 ggt agc aat atg aca att gaa tgc aaa ttc cca gta gaa aaa caa tta      202
46 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
47 35 40 45
49 gac ctg gct gca cta att gtc tat tgg gaa atg gag gat aag aac att      250
50 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
51 50 55 60
53 att caa ttt gtg cat gga gag gaa gac ctg aag gtt cag cat agt agc      298
54 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
55 65 70 75 80
57 tac aga cag agg gcc cgg ctg ttg aag gac cag ctc tcc ctg gga aat      346
58 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
59 85 90 95
61 gct gca ctt cag atc aca gat gtg aaa ttg cag gat gca ggg gtg tac      394
62 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
63 100 105 110
65 cgc tgc atg atc agc tat ggt ggt gcc gac tac aag cga att act gtg      442
66 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
67 115 120 125

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69 aaa gtc aat gcc cca tac aac aaa atc aac caa aga att ttg gtt gtg 490
70 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
71      130                      135                      140
73 gat cca gtc acc tct gaa cat gaa ctg aca tgt cag gct gag ggc tac 538
74 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
75 145                      150                      155                      160
77 ccc aag gcc gaa gtc atc tgg aca agc agt gac cat caa gtc ctg agt 586
78 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
79      165                      170                      175
81 ggt aag acc acc acc acc aat tcc aag aga gag gag aag ctt ttc aat 634
82 Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
83      180                      185                      190
85 gtg acc agc aca ctg aga atc aac aca aca act aat gag att ttc tac 682
86 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
87      195                      200                      205
89 tgc act ttt agg aga tta gat cct gag gaa aac cat aca gct gaa ttg 730
90 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
91      210                      215                      220
93 gtc atc cca ggt aat att ctg aat gtg tcc att aaa ata tgt cta aca 778
94 Val Ile Pro Gly Asn Ile Leu Asn Val Ser Ile Lys Ile Cys Leu Thr
95 225                      230                      235                      240
97 ctg tcc cct agc acc tagcatgatg tctgcctatc atagtcattc agtgattgtt 833
98 Leu Ser Pro Ser Thr
99      245
101 gaataaatga atgaatgaat aacactatgt ttacaaaata taccctaatt cctcacctcc 893
103 attcatccaa accatattgt tacttaataa acattcagca gatatttatg gaataaaaaa 953
105 aaaaaaaaaa aaaaaa 968
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109 <211> LENGTH: 245
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 2
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115 1 5 10 15
117 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
118 20 25 30
120 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
121 35 40 45
123 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
124 50 55 60
126 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
127 65 70 75 80
129 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
130 85 90 95
132 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
133 100 105 110
135 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
136 115 120 125
138 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val

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139      130      135      140
141 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
142 145      150      155      160
144 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
145      165      170      175
147 Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
148      180      185      190
150 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
151      195      200      205
153 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
154      210      215      220
156 Val Ile Pro Gly Asn Ile Leu Asn Val Ser Ile Lys Ile Cys Leu Thr
157 225      230      235      240
159 Leu Ser Pro Ser Thr
160      245
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164 <211> LENGTH: 1553
165 <212> TYPE: DNA
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170 <222> LOCATION: (53)..(922)
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174                                     Met Arg
175                                     1
177 ata ttt gct gtc ttt ata ttc atg acc tac tgg cat ttg ctg aac gca 106
178 Ile Phe Ala Val Phe Ile Phe Met Thr Tyr Trp His Leu Leu Asn Ala
179      5      10      15
181 ttt act gtc acg gtt ccc aag gac cta tat gtg gta gag tat ggt agc 154
182 Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr Gly Ser
183      20      25      30
185 aat atg aca att gaa tgc aaa ttc cca gta gaa aaa caa tta gac ctg 202
186 Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu Asp Leu
187 35      40      45      50
189 gct gca cta att gtc tat tgg gaa atg gag gat aag aac att att caa 250
190 Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile Ile Gln
191      55      60      65
193 ttt gtg cat gga gag gaa gac ctg aag gtt cag cat agt agc tac aga 298
194 Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser Tyr Arg
195      70      75      80
197 cag agg gcc cgg ctg ttg aag gac cag ctc tcc ctg gga aat gct gca 346
198 Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn Ala Ala
199      85      90      95
201 ctt cag atc aca gat gtg aaa ttg cag gat gca ggg gtg tac cgc tgc 394
202 Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr Arg Cys
203      100      105      110
205 atg atc agc tat ggt ggt gcc gac tac aag cga att act gtg aaa gtc 442
206 Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val Lys Val

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207 115          120          125          130
209 aat gcc cca tac aac aaa atc aac caa aga att ttg gtt gtg gat cca 490
210 Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val Asp Pro
211          135          140          145
213 gtc acc tct gaa cat gaa ctg aca tgt cag gct gag ggc tac ccc aag 538
214 Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr Pro Lys
215          150          155          160
217 gcc gaa gtc atc tgg aca agc agt gac cat caa gtc ctg agt ggt aag 586
218 Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser Gly Lys
219          165          170          175
221 acc acc acc acc aat tcc aag aga gag gag aag ctt ttc aat gtg acc 634
222 Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn Val Thr
223          180          185          190
225 agc aca ctg aga atc aac aca aca act aat gag att ttc tac tgc act 682
226 Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr Cys Thr
227 195          200          205          210
229 ttt agg aga tta gat cct gag gaa aac cat aca gct gaa ttg gtc atc 730
230 Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu Val Ile
231          215          220          225
233 cca gaa cta cct ctg gca cat cct cca aat gaa agg act cac ttg gta 778
234 Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His Leu Val
235          230          235          240
237 att ctg gga gcc atc tta tta tgc ctt ggt gta gca ctg aca ttc atc 826
238 Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr Phe Ile
239          245          250          255
241 ttc cgt tta aga aaa ggg aga atg atg gat gtg aaa aaa tgt ggc atc 874
242 Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys Gly Ile
243          260          265          270
245 caa gat aca aac tca aag aag caa agt gat aca cat ttg gag gag acg 922
246 Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu Glu Thr
247 275          280          285          290
249 taatccagca ttggaacttc tgaatcttcaa gcaggggattc tcaacctgtg gtttaggggt 982
251 tcatcggggc tgagcgtgac aagaggaagg aatgggcccg tgggatgcag gcaatgtggg 1042
253 acttaaaagg cccaagcact gaaaatggaa cctggcgaaa gcagaggagg agaatgaaga 1102
255 aagatggagt caaacaggga gcctggaggg agaccttgat actttcaaat gcctgagggg 1162
257 ctcatcgacg cctgtgacag ggagaaagga tactttotgaa caaggagcct ccaagcaaat 1222
259 catccattgc tcatcctagg aagacgggtt gagaatccct aatttgaggg tcagttcctg 1282
261 cagaagtgcc ctttgccctcc actcaatgcc tcaatttggt ttctgcatga ctgagagtct 1342
263 cagtgttgga acgggacagt atttatgtat gagtttttcc tattttatattt gagtctgtga 1402
265 ggtcttcttg tcatgtgagt gtggttggtga atgatttctt ttgaagatat attgtagtag 1462
267 atgttacaat tttgtcgcca aactaaactt gctgcttaat gatttgctca catctagtaa 1522
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273 <211> LENGTH: 290
274 <212> TYPE: PRT
275 <213> ORGANISM: Homo sapiens
277 <400> SEQUENCE: 4
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279 1 5 10 15

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281 Asn Ala Phe Thr Val Thr Val Pro Lys Asp Leu Tyr Val Val Glu Tyr
282          20          25          30
284 Gly Ser Asn Met Thr Ile Glu Cys Lys Phe Pro Val Glu Lys Gln Leu
285          35          40          45
287 Asp Leu Ala Ala Leu Ile Val Tyr Trp Glu Met Glu Asp Lys Asn Ile
288          50          55          60
290 Ile Gln Phe Val His Gly Glu Glu Asp Leu Lys Val Gln His Ser Ser
291          65          70          75          80
293 Tyr Arg Gln Arg Ala Arg Leu Leu Lys Asp Gln Leu Ser Leu Gly Asn
294          85          90          95
296 Ala Ala Leu Gln Ile Thr Asp Val Lys Leu Gln Asp Ala Gly Val Tyr
297          100         105         110
299 Arg Cys Met Ile Ser Tyr Gly Gly Ala Asp Tyr Lys Arg Ile Thr Val
300          115         120         125
302 Lys Val Asn Ala Pro Tyr Asn Lys Ile Asn Gln Arg Ile Leu Val Val
303          130         135         140
305 Asp Pro Val Thr Ser Glu His Glu Leu Thr Cys Gln Ala Glu Gly Tyr
306          145         150         155         160
308 Pro Lys Ala Glu Val Ile Trp Thr Ser Ser Asp His Gln Val Leu Ser
309          165         170         175
311 Gly Lys Thr Thr Thr Thr Asn Ser Lys Arg Glu Glu Lys Leu Phe Asn
312          180         185         190
314 Val Thr Ser Thr Leu Arg Ile Asn Thr Thr Thr Asn Glu Ile Phe Tyr
315          195         200         205
317 Cys Thr Phe Arg Arg Leu Asp Pro Glu Glu Asn His Thr Ala Glu Leu
318          210         215         220
320 Val Ile Pro Glu Leu Pro Leu Ala His Pro Pro Asn Glu Arg Thr His
321          225         230         235         240
323 Leu Val Ile Leu Gly Ala Ile Leu Leu Cys Leu Gly Val Ala Leu Thr
324          245         250         255
326 Phe Ile Phe Arg Leu Arg Lys Gly Arg Met Met Asp Val Lys Lys Cys
327          260         265         270
329 Gly Ile Gln Asp Thr Asn Ser Lys Lys Gln Ser Asp Thr His Leu Glu
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332 Glu Thr
333          290
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336 <211> LENGTH: 24
337 <212> TYPE: DNA
338 <213> ORGANISM: Homo sapiens
340 <400> SEQUENCE: 5
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344 <211> LENGTH: 25
345 <212> TYPE: DNA
346 <213> ORGANISM: Homo sapiens
348 <400> SEQUENCE: 6
349 aggtgctagg ggacagtgtt agaca
351 <210> SEQ ID NO: 7

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25

VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12112001\I002775.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:357 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:  
L:365 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE: